NCBI Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]
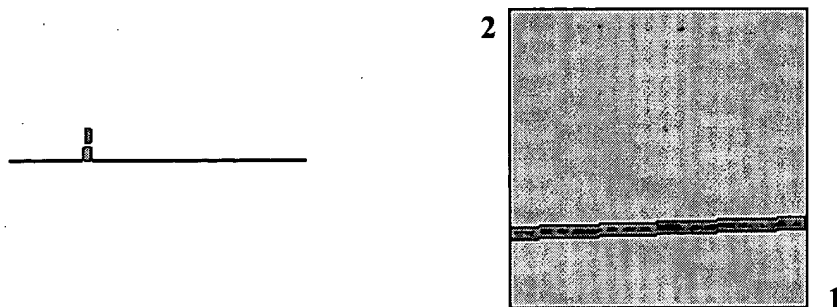
Match: [1] Mismatch: [-2] gap open: [5] gap extension: [2]
x_dropoff: [50] expect: [10.0] wordsize: [11] Filter ☑ [Align]

Sequence 1 lcl|seq_1   **Length** 117   (1 .. 117)

Sequence 2 gi 307165 Human myeloid cell differentiation protein (MCL1) mRNA.   **Length** 3934 (1 .. 3934)

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

```
Score =  225 bits. (117), Expect = 1e-56
Identities = 117/117 (100%)
 Strand = Plus / Plus
```



```
Query: 1     gatgggtttgtggagttcttccatgtagaggacctagaaggtggcatcaggaatgtgctg 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 997   gatgggtttgtggagttcttccatgtagaggacctagaaggtggcatcaggaatgtgctg 1056

Query: 61    ctggcttttgcaggtgttgctggagtaggagctggtttggcatatctaataagatag 117
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1057  ctggcttttgcaggtgttgctggagtaggagctggtttggcatatctaataagatag 1113
```

```
CPU time:     0.02 user secs.        0.00 sys. secs        0.02 total secs.

Lambda      K        H
   1.33     0.621     1.12

Gapped
Lambda      K        H
   1.33     0.621     1.12

Matrix: blastn matrix:1 -2
```

```
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 1
Number of Sequences: 0
Number of extensions: 1
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 117
length of database: 8,612,495,175
effective HSP length: 23
effective length of query: 94
effective length of database: 8,612,495,152
effective search space: 809574544288
effective search space used: 809574544288
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 19 (37.2 bits)
```

NCBI

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BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match: [1] Mismatch: [-2] gap open: [5] gap extension: [2]
x_dropoff: [50] expect: [10.0] wordsize: [11] Filter ☑ [Align]

Sequence 1 lcl|seq_1   **Length** 688   (1 .. 688)

Sequence 2 gi 307165   Human myeloid cell differentiation protein (MCL1) mRNA.   **Length** 3934 (1 .. 3934)
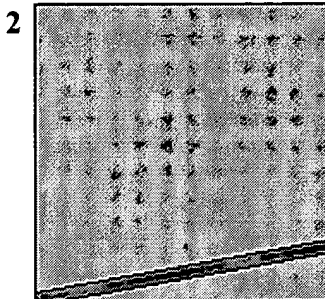
NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

```
Score = 1285 bits (668), Expect = 0.0
Identities = 679/688 (98%)
 Strand = Plus / Plus
```



```
Query: 1    atgtttggcctcaaaagaaacgcggtaatcggactcaacctctactgtnnnnnnnccggc  60
            |||||||||||||||||||||||||||||||||||||||||||||||||       |||||
Sbjct: 61   atgtttggcctcaaaagaaacgcggtaatcggactcaacctctactgtggggggccggc  120


Query: 61   ttggggggccggcagcggcggcgccacccgcccgggagggcgacttttggctacggagaag  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121  ttggggggccggcagcggcggcgccacccgcccgggagggcgacttttggctacggagaag  180


Query: 121  gaggcctcggcccggcgagagatagggggagggggaggccggcgcggtgattggcggaagc  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181  gaggcctcggcccggcgagagatagggggagggggaggccggcgcggtgattggcggaagc  240


Query: 181  gccggcgcaagccccccgtccaccctcacgccagactcccggagggtcgcgcggccgccg  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241  gccggcgcaagccccccgtccaccctcacgccagactcccggagggtcgcgcggccgccg  300
```

```
Query:  241  cccattggcgccgaggtccccgacgtcaccgcgaccccgcgaggctgcttttcttcgcg  300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  301  cccattggcgccgaggtccccgacgtcaccgcgaccccgcgaggctgcttttcttcgcg  360


Query:  301  cccacccgccgcgcggcgccgcttgaggagatggaagccccggccgctgacgccatcatg  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  361  cccacccgccgcgcggcgccgcttgaggagatggaagccccggccgctgacgccatcatg  420


Query:  361  tcgcccgaagaggagctggacgggtacgagccggagcctctcgggaagcggccggctgtc  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  421  tcgcccgaagaggagctggacgggtacgagccggagcctctcgggaagcggccggctgtc  480


Query:  421  ctgccgctgctggagttggtcggggaatctggtaataacaccagtacggacgggtcacta  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  481  ctgccgctgctggagttggtcggggaatctggtaataacaccagtacggacgggtcacta  540


Query:  481  ccctcgacgccgccgccagcagaggaggaggaggacgacttgtaccggcagtcgctggag  540
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct:  541  ccctcgacgccgccgccagcagaggaggaggaggacgagttgtaccggcagtcgctggag  600


Query:  541  attatctctcggtaccttcgggagcaggccaccggcgccaaggacacaaagccaatgggc  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  601  attatctctcggtaccttcgggagcaggccaccggcgccaaggacacaaagccaatgggc  660


Query:  601  aggtctggggccaccagcaggaaggcgctggagaccttacgacgggttggggatggcgtg  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  661  aggtctggggccaccagcaggaaggcgctggagaccttacgacgggttggggatggcgtg  720


Query:  661  cagcgcaaccacgagacggccttccaag  688
             ||||||||||||||||||||| |||||||
Sbjct:  721  cagcgcaaccacgagacggtcttccaag  748
```

CPU time: 0.02 user secs.   0.00 sys. secs   0.02 total secs.

Lambda   K   H
   1.33   0.621   1.12

Gapped
Lambda   K   H
   1.33   0.621   1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 5
Number of Sequences: 0
Number of extensions: 5
Number of successful extensions: 3
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 688
length of database: 8,612,495,175
effective HSP length: 24
effective length of query: 664
effective length of database: 8,612,495,151

```
effective search space: 5718696780264
effective search space used: 5718696780264
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 20 (39.1 bits)
```

 Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2
x_dropoff: 50 expect: 10.0 wordsize: 11 Filter ☑ Align

Sequence 1 lcl|seq_1   **Length** 248 (1 .. 248)

Sequence 2 gi 307165 Human myeloid cell differentiation protein (MCL1) mRNA.   **Length** 3934 (1 .. 3934)
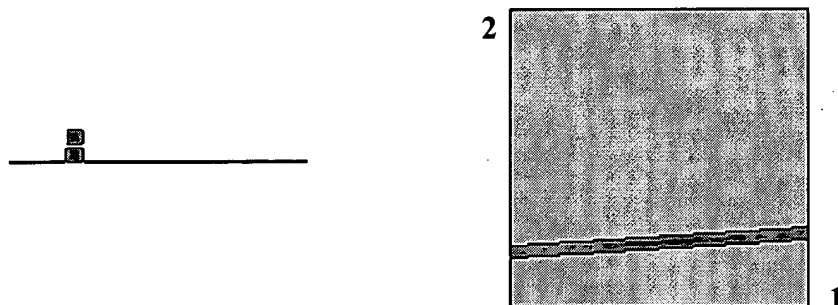
NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

```
Score =  477 bits (248), Expect = e-132
Identities = 248/248 (100%)
 Strand = Plus / Plus
```



```
Query: 1    gcatgcttcggaaactggacatcaaaaacgaagacgatgtgaaatcgttgtctcgagtga 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 749  gcatgcttcggaaactggacatcaaaaacgaagacgatgtgaaatcgttgtctcgagtga 808


Query: 61   tgatccatgttttcagcgacggcgtaacaaactggggcaggattgtgactctcatttctt 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 809  tgatccatgttttcagcgacggcgtaacaaactggggcaggattgtgactctcatttctt 868


Query: 121  ttggtgcctttgtggctaaacacttgaagaccataaaccaagaaagctgcatcgaaccat 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 869  ttggtgcctttgtggctaaacacttgaagaccataaaccaagaaagctgcatcgaaccat 928


Query: 181  tagcagaaagtatcacagacgttctcgtaaggacaaaacgggactggctagttaaacaaa 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 929  tagcagaaagtatcacagacgttctcgtaaggacaaaacgggactggctagttaaacaaa 988
```

```
Query: 241 gaggctgg 248
            ||||||||
Sbjct: 989 gaggctgg 996
```

CPU time: 0.02 user secs.   0.01 sys. secs   0.03 total secs.

Lambda   K   H
    1.33   0.621   1.12

Gapped
Lambda   K   H
    1.33   0.621   1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 1
Number of Sequences: 0
Number of extensions: 1
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 248
length of database: 8,612,495,175
effective HSP length: 24
effective length of query: 224
effective length of database: 8,612,495,151
effective search space: 1929198913824
effective search space used: 1929198913824
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 20 (39.1 bits)
```